

SEQUENCE LISTING

<110> Lye, Stephen
Dong, Xuesen

<120> METHODS AND COMPOSITIONS FOR MODULATING A STEROID RECEPTOR

<130> MTS6USA

<140> PCT/CA2005/000042
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<170> PatentIn version 3.3

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35 40 45

Pro Gly Pro Gly Gln Ser Gly Pro Lys Pro Pro Ile Pro Pro Pro Pro
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Pro His Gln Gln Gln Gln Gln Pro Pro Pro Gln Gln Pro Pro Pro Gln
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Gln Pro Pro Pro His Gln Pro Pro Pro His Pro Gln Pro His Gln Gln
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Gln Gln Pro Pro Pro Pro Pro Gln Asp Ser Ser Lys Pro Val Val Ala
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 Gln Gly Pro Gly Pro Ala Pro Gly Val Gly Ser Ala Pro Pro Ala Ser
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 Pro Arg Gly Gly Arg Gln His His Pro Pro Tyr His Gln Gln His His
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 Pro Ala Asp Ile Thr Glu Asp Glu Phe Lys Arg Leu Phe Ala Lys Tyr
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 Gly Glu Pro Gly Glu Val Phe Ile Asn Lys Gly Lys Gly Phe Gly Phe
 325 330 335
 Ile Lys Leu Glu Ser Arg Ala Leu Ala Glu Ile Ala Lys Ala Glu Leu
 340 345 350

Asp Asp Thr Pro Met Arg Gly Arg Gln Leu Arg Val Arg Phe Ala Thr
 Page 2

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Glu	Leu	Leu	Glu	Glu	Ala	Phe	Ser	Gln	Phe	Gly	Pro	Ile	Glu	Arg	Ala
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Val	Val	Ile	Val	Asp	Asp	Arg	Gly	Arg	Ser	Thr	Gly	Lys	Gly	Ile	Val
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35 40 45

Pro Gly Pro Gly Gln Ser Gly Pro Lys Pro Pro Ile Pro Pro Pro Pro
50 55 60

Pro His Gln Gln Gln Gln Gln Pro Pro Pro Gln Gln Pro Pro Pro Gln
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Gln Pro Pro Pro His Gln Pro Pro Pro His Pro Gln Pro His Gln Gln
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Gln Gln Pro Pro Pro Pro Pro Gln Asp Ser Ser Lys Pro Val Val Ala
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 Gln Gly Pro Pro Pro Gly Gly Pro Gly Gly Arg Ser Glu Glu Lys Ile
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 Ser Asp Ser Glu Gly Phe Lys Ala Asn Leu Ser Leu Leu Arg Arg Pro
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 Ile Lys Leu Glu Ser Arg Ala Leu Ala Glu Ile Ala Lys Ala Glu Leu
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His Ala Ala Ala Leu Ser Val Arg Asn Leu Ser Pro Tyr Val Ser Asn
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Val Val Ile Val Asp Asp Arg Gly Arg Ser Thr Gly Lys Gly Ile Val
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Glu Gly Val Phe Leu Leu Thr Thr Thr Pro Arg Pro Val Ile Val Glu
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Glu Leu Arg Arg Met Glu Glu Leu His Asn Gln Glu Met Gln Lys Arg
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 Gln Pro Pro Pro His Gln Pro Pro Pro His Pro Gln Pro His Gln Gln
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 Gln Gln Pro Pro Pro Pro Pro Gln Asp Ser Ser Lys Pro Val Val Ala
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 Gly Gly Lys Met Pro Gly Gly Pro Lys Pro Gly Gly Gly Pro Gly Leu
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 Gln Gly Pro Pro Pro Gly Gly Pro Gly Gly Arg Ser Glu Glu Lys Ile
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 Ser Asp Ser Glu Gly Phe Lys Ala Asn Leu Ser Leu Leu Arg Arg Pro
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 Gly Glu Lys Thr Tyr Thr Gln Arg Cys Arg Leu Phe Val Gly Asn Leu
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 Pro Ala Asp Ile Thr Glu Asp Glu Phe Lys Arg Leu Phe Ala Lys Tyr
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 Gly Glu Pro Gly Glu Val Phe Ile Asn Lys Gly Lys Gly Phe Gly Phe
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 Asp Asp Thr Pro Met Arg Gly Arg Gln Leu Arg Val Arg Phe Ala Thr
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 His Ala Ala Ala Leu Ser Val Arg Asn Leu Ser Pro Tyr Val Ser Asn
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 Glu Gly Val Phe Leu Leu Thr Thr Thr Pro Arg Pro Val Ile Val Glu
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 Gly Ser Gly Gly Gln Lys Phe Pro Pro Leu Gly Gly Gly Gly Ile
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Gly Ser Ala Pro Pro Ala Ser Ser Ser Ala Pro Pro Ala Thr Pro Pro
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Thr Ser Gly Ala Pro Pro Gly Ser Gly Pro Gly Pro Thr Pro Thr Pro
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Pro Pro Ala Val Thr Ser Ala Pro Pro Gly Ala Pro Pro Pro Thr Pro
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Pro Pro Pro Ala Ala Val Pro Gly Pro Gly Pro Gly Pro Lys Gln Gly
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Pro Gly Pro Gly Gly Pro Lys Gly Gly Lys Met Pro Gly Gly Pro Lys
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Pro Gly Gly Gly Pro Gly Leu Ser Thr Pro Gly Gly His Pro Lys Pro
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Pro His Arg Gly Gly Gly Glu Pro Arg Gly Gly Arg Gln His His Pro
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Pro Tyr His Gln Gln His His Gln Gly Pro Pro Pro Gly Gly Pro Gly
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Gly Arg Ser Glu Glu Lys Ile Ser Asp Ser Glu Gly Phe Lys Ala Asn
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 Lys Arg Leu Phe Ala Lys Tyr Gly Glu Pro Gly Glu Val Phe Ile Asn
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 Lys Gly Lys Gly Phe Gly Phe Ile Lys Leu Glu Ser Arg Ala Leu Ala
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 Glu Ile Ala Lys Ala Glu Leu Asp Asp Thr Pro Met Arg Gly Arg Gln
 275 280 285
 Leu Arg Val Arg Phe Ala Thr His Ala Ala Ala Leu Ser Val Arg Asn
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 Leu Ser Pro Tyr Val Ser Asn Glu Leu Leu Glu Glu Ala Phe Ser Gln
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 Lys Ala Phe Glu Arg Cys Ser Glu Gly Val Phe Leu Leu Thr Thr Thr
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 Tyr Ser Gln Arg Trp Lys Ser Leu Asp Glu Met Glu Lys Gln Gln Arg
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Glu Arg Arg Arg Arg Glu Glu Glu Met Met Ile Arg Gln Arg Glu Met
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Tyr Met Asp Pro Arg Glu Arg Asp Met Arg Met Gly Gly Gly Gly Ala
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Met Asn Met Gly Asp Pro Tyr Gly Ser Gly Gly Gln Lys Phe Pro Pro
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Pro Ala Thr Met Ser Gly Ser Met Met Gly Ser Asp Met Arg Thr Glu
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Arg Phe Gly Gln Gly Gly Ala Gly Pro Val Gly Gly Gln Gly Pro Arg
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 Pro Gly₅₀ Pro Gly Gln Ser Gly₅₅ Pro Lys Pro Pro Ile₆₀ Pro Pro Pro Pro
 Pro His Gln Gln Gln₇₀ Gln Gln Pro Pro Pro Gln₇₅ Gln Pro Pro Pro Gln₈₀
 Gln Pro Pro Pro His₈₅ Gln Pro Pro Pro His₉₀ Pro Gln Pro His₉₅ Gln Gln
 Gln Gln Pro Pro₁₀₀ Pro Pro Pro Gln Asp₁₀₅ Ser Ser Lys Pro Val₁₁₀ Val Ala
 Gln Gly Pro₁₁₅ Gly Pro Ala Pro Gly₁₂₀ Val Gly Ser Ala Pro₁₂₅ Pro Ala Ser
 Ser Ser₁₃₀ Ala Pro Pro Ala Thr₁₃₅ Pro Pro Thr Ser Gly₁₄₀ Ala Pro Pro Gly
 Ser Gly₁₄₅ Pro Gly Pro Thr₁₅₀ Pro Thr Pro Pro Pro Ala Val Thr Ser Ala₁₆₀
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 Gly Pro Gly₁₉₅ Pro Gly Pro Lys Gln₂₀₀ Gly Pro Gly Pro Gly₂₀₅ Gly Pro Lys
 Gly Gly₂₁₀ Lys Met Pro Gly Gly₂₁₅ Pro Lys Pro Gly Gly₂₂₀ Gly Pro Gly Leu
 Ser Thr Pro Gly Gly His₂₃₀ Pro Lys Pro Pro His₂₃₅ Arg Gly Gly Gly Glu₂₄₀
 Pro Arg Gly Gly Arg₂₄₅ Gln His His Pro₂₅₀ Tyr His Gln Gln His₂₅₅ His
 Gln Gly Pro Pro₂₆₀ Pro Gly Gly Pro Gly₂₆₅ Gly Arg Ser Glu Glu₂₇₀ Lys Ile
 Ser Asp Ser₂₇₅ Glu Gly Phe Lys Ala₂₈₀ Asn Leu Ser Leu Leu₂₈₅ Arg Arg Pro
 Gly Glu Lys Thr Tyr Thr Gln Arg Cys Arg Leu Phe Val Gly Asn Leu

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	Glu Ile Ala Lys Ala 350	Glu Leu
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	Tyr Val Ser Asn	
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Val Val Ile Val	Asp 405	Asp Arg Gly Arg Ser 410
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	Ile Val Glu	
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	Glu Lys Leu Ala	
Gln 465	Lys Asn Pro Met Tyr 470	Gln Lys Glu Arg Glu 475
	Thr Pro Pro Arg Phe 480	
Ala Gln His Gly	Thr 485	Phe Glu Tyr Glu Tyr 490
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Lys Glu Arg Glu Thr Pro Pro Arg Phe Ala Gln His Gly Thr Phe Glu
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 35 40 45

Ser Ala Ile Pro Ile Ser Leu Asp Gly Leu Leu Phe Pro Arg Pro Cys
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 Gln Gly Gln Asp Pro Ser Asp Glu Lys Thr Gln Asp Gln Gln Ser Leu
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 Ser Asp Val Glu Gly Ala Tyr Ser Arg Ala Glu Ala Thr Arg Gly Ala
 85 90 95
 Gly Gly Ser Ser Ser Ser Pro Pro Glu Lys Asp Ser Gly Leu Leu Asp
 100 105 110
 Ser Val Leu Asp Thr Leu Leu Ala Pro Ser Gly Pro Gly Gln Ser Gln
 115 120 125
 Pro Ser Pro Pro Ala Cys Glu Val Thr Ser Ser Trp Cys Leu Phe Gly
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 Pro Glu Leu Pro Glu Asp Pro Pro Ala Ala Pro Ala Thr Gln Arg Val
 145 150 155 160
 Leu Ser Pro Leu Met Ser Arg Ser Gly Cys Lys Val Gly Asp Ser Ser
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 Gly Thr Ala Ala Ala His Lys Val Leu Pro Arg Gly Leu Ser Pro Ala
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 Arg Gln Leu Leu Leu Pro Ala Ser Glu Ser Pro His Trp Ser Gly Ala
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 Pro Val Lys Pro Ser Pro Gln Ala Ala Ala Val Glu Val Glu Glu Glu
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 Asp Ser Ser Glu Ser Glu Glu Ser Ala Gly Pro Leu Leu Lys Gly Lys
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 Pro Arg Ala Leu Gly Gly Ala Ala Ala Gly Gly Gly Ala Ala Ala Cys
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 Pro Pro Gly Ala Ala Ala Gly Gly Val Ala Leu Val Pro Lys Glu Asp
 260 265 270
 Ser Arg Phe Ser Ala Pro Arg Val Ala Leu Val Glu Gln Asp Ala Pro
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His Val Pro Ile Leu Pro Leu Asn His Ala Leu Leu Ala Ala Arg Thr
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 Arg Gln Leu Leu Glu Asp Glu Ser Tyr Asp Gly Gly Ala Gly Ala Ala
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 Val Ala Val Gly Asp Phe Pro Asp Cys Ala Tyr Pro Pro Asp Ala Glu
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 Pro Lys Asp Asp Ala Tyr Pro Leu Tyr Ser Asp Phe Gln Pro Pro Ala
 370 375 380
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 Pro Arg Ser Tyr Leu Val Ala Gly Ala Asn Pro Ala Ala Phe Pro Asp
 405 410 415
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 420 425 430
 Arg Pro Gly Glu Ala Ala Val Thr Ala Ala Pro Ala Ser Ala Ser Val
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 465 470 475 480
 Lys Ala Pro Gly Ala Ser Gly Cys Leu Leu Pro Arg Asp Gly Leu Pro
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 Ser Thr Ser Ala Ser Ala Ala Ala Ala Gly Ala Ala Pro Ala Leu Tyr
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 Pro Ala Leu Gly Leu Asn Gly Leu Pro Gln Leu Gly Tyr Gln Ala Ala
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 Val Leu Lys Glu Gly Leu Pro Gln Val Tyr Pro Pro Tyr Leu Asn Tyr
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Ser Leu Pro Gln Lys Ile Cys Leu Ile Cys Gly Asp Glu Ala Ser Gly

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Cys	Ile 610	Val	Asp	Lys	Ile	Arg 615	Arg	Lys	Asn	Cys	Pro 620	Ala	Cys	Arg	Leu
Arg 625	Lys	Cys	Cys	Gln	Ala 630	Gly	Met	Val	Leu	Gly 635	Gly	Arg	Lys	Phe	Lys 640
Lys	Phe	Asn	Lys	Val 645	Arg	Val	Val	Arg	Ala 650	Leu	Asp	Ala	Val	Ala 655	Leu
Pro	Gln	Pro	Leu 660	Gly	Val	Pro	Asn	Glu 665	Ser	Gln	Ala	Leu	Ser	Gln	Arg
Phe	Thr	Phe 675	Ser	Pro	Gly	Gln	Asp 680	Ile	Gln	Leu	Ile	Pro 685	Pro	Leu	Ile
Asn	Leu 690	Leu	Met	Ser	Ile	Glu 695	Pro	Asp	Val	Ile	Tyr 700	Ala	Gly	His	Asp
Asn 705	Thr	Lys	Pro	Asp	Thr 710	Ser	Ser	Ser	Leu	Leu 715	Thr	Ser	Leu	Asn	Gln 720
Leu	Gly	Glu	Arg	Gln 725	Leu	Leu	Ser	Val	Val 730	Lys	Trp	Ser	Lys	Ser 735	Leu
Pro	Gly	Phe	Arg 740	Asn	Leu	His	Ile	Asp 745	Asp	Gln	Ile	Thr	Leu 750	Ile	Gln
Tyr	Ser	Trp 755	Met	Ser	Leu	Met	Val 760	Phe	Gly	Leu	Gly	Trp 765	Arg	Ser	Tyr
Lys	His 770	Val	Ser	Gly	Gln	Met 775	Leu	Tyr	Phe	Ala	Pro 780	Asp	Leu	Ile	Leu
Asn 785	Glu	Gln	Arg	Met	Lys 790	Glu	Ser	Ser	Phe	Tyr 795	Ser	Leu	Cys	Leu	Thr 800
Met	Trp	Gln	Ile	Pro 805	Gln	Glu	Phe	Val	Lys 810	Leu	Gln	Val	Ser	Gln 815	Glu
Glu	Phe	Leu	Cys 820	Met	Lys	Val	Leu	Leu	Leu	Leu	Asn	Thr	Ile 830	Pro	Leu

Glu Gly Leu Arg Ser Gln Thr Gln Phe Glu Glu Met Arg Ser Ser Tyr
835 840 845

Ile Arg Glu Leu Ile Lys Ala Ile Gly Leu Arg Gln Lys Gly Val Val
850 855 860

Ser Ser Ser Gln Arg Phe Tyr Gln Leu Thr Lys Leu Leu Asp Asn Leu
865 870 875 880

His Asp Leu Val Lys Gln Leu His Leu Tyr Cys Leu Asn Thr Phe Ile
885 890 895

Gln Ser Arg Ala Leu Ser Val Glu Phe Pro Glu Met Met Ser Glu Val
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Ile Ala Ala Gln Leu Pro Lys Ile Leu Ala Gly Met Val Lys Pro Leu
915 920 925

Leu Phe His Lys Lys
930

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35 40 45

Ser Ala Ile Pro Ile Ser Leu Asp Gly Leu Leu Phe Pro Arg Pro Cys
50 55 60

Gln Gly Gln Asp Pro Ser Asp Glu Lys Thr Gln Asp Gln Gln Ser Leu
65 70 75 80

Ser Asp Val Glu Gly Ala Tyr Ser Arg Ala Glu Ala Thr Arg Gly Ala
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Gly Gly Ser Ser Ser Ser Pro Pro Glu Lys Asp Ser Gly Leu Leu Asp
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 Ser Val Leu Asp Thr Leu Leu Ala Pro Ser Gly Pro Gly Gln Ser Gln
 115 120 125
 Pro Ser Pro Pro Ala Cys Glu Val Thr Ser Ser Trp Cys Leu Phe Gly
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 Pro Glu Leu Pro Glu Asp Pro Pro Ala Ala Pro Ala Thr Gln Arg Val
 145 150 155 160
 Leu Ser Pro Leu Met Ser Arg Ser Gly Cys Lys Val Gly Asp Ser Ser
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 Gly Thr Ala Ala Ala His Lys Val Leu Pro Arg Gly Leu Ser Pro Ala
 180 185 190
 Arg Gln Leu Leu Leu Pro Ala Ser Glu Ser Pro His Trp Ser Gly Ala
 195 200 205
 Pro Val Lys Pro Ser Pro Gln Ala Ala Ala Val Glu Val Glu Glu Glu
 210 215 220
 Asp Gly Ser Glu Ser Glu Glu Ser Ala Gly Pro Leu Leu Lys Gly Lys
 225 230 235 240
 Pro Arg Ala Leu Gly Gly Ala Ala Ala Gly Gly Gly Ala Ala Ala Val
 245 250 255
 Pro Pro Gly Ala Ala Ala Gly Gly Val Ala Leu Val Pro Lys Glu Asp
 260 265 270
 Ser Arg Phe Ser Ala Pro Arg Val Ala Leu Val Glu Gln Asp Ala Pro
 275 280 285
 Met Ala Pro Gly Arg Ser Pro Leu Ala Thr Thr Val Met Asp Phe Ile
 290 295 300
 His Val Pro Ile Leu Pro Leu Asn His Ala Leu Leu Ala Ala Arg Thr
 305 310 315 320
 Arg Gln Leu Leu Glu Asp Glu Ser Tyr Asp Gly Gly Ala Gly Ala Ala
 325 330 335
 Ser Ala Phe Ala Pro Pro Arg Ser Ser Pro Cys Ala Ser Ser Thr Pro
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Val Ala Val Gly Asp Phe Pro Asp Cys Ala Tyr Pro Pro Asp Ala Glu
355 360 365
Pro Lys Asp Asp Ala Tyr Pro Leu Tyr Ser Asp Phe Gln Pro Pro Ala
370 375 380
Leu Lys Ile Lys Glu Glu Glu Glu Gly Ala Glu Ala Ser Ala Arg Ser
385 390 395 400
Pro Arg Ser Tyr Leu Val Ala Gly Ala Asn Pro Ala Ala Phe Pro Asp
405 410 415
Phe Pro Leu Gly Pro Pro Pro Pro Leu Pro Pro Arg Ala Thr Pro Ser
420 425 430
Arg Pro Gly Glu Ala Ala Val Thr Ala Ala Pro Ala Ser Ala Ser Val
435 440 445
Ser Ser Ala Ser Ser Ser Gly Ser Thr Leu Glu Cys Ile Leu Tyr Lys
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Ala Glu Gly Ala Pro Pro Gln Gln Gly Pro Phe Ala Pro Pro Pro Cys
465 470 475 480
Lys Ala Pro Gly Ala Ser Gly Cys Leu Leu Pro Arg Asp Gly Leu Pro
485 490 495
Ser Thr Ser Ala Ser Ala Ala Ala Ala Gly Ala Ala Pro Ala Leu Tyr
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Pro Ala Leu Gly Leu Asn Gly Leu Pro Gln Leu Gly Tyr Gln Ala Ala
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530 535 540
Leu Arg Pro Asp Ser Glu Ala Ser Gln Ser Pro Gln Tyr Ser Phe Glu
545 550 555 560
Ser Leu Pro Gln Lys Ile Cys Leu Ile Cys Gly Asp Glu Ala Ser Gly
565 570 575
Cys His Tyr Gly Val Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Lys
580 585 590
Arg Ala Met Glu Gly Gln His Asn Tyr Leu Cys Ala Gly Arg Asn Asp
595 600 605
Cys Ile Val Asp Lys Ile Arg Arg Lys Asn Cys Pro Ala Cys Arg Leu

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	Gly Phe Arg Asn Leu 640	
His 645	Ile Asp Asp Gln 645	Ile Thr Leu Ile Gln 650
	Tyr Ser Trp Met Ser Leu 655	
Met 660	Val Phe Gly 660	Leu Gly Trp Arg Ser 665
	Tyr Lys His Val Ser 670	Gly Gln
Met 675	Leu Tyr Phe Ala Pro Asp 680	Ile Leu Asn Glu 685
	Arg Met Lys	
Glu 690	Ser Ser Phe Tyr Ser 695	Leu Cys Leu Thr Met 700
	Trp Gln Ile Pro Gln	
Glu 705	Phe Val Lys Leu Gln 710	Val Ser Gln Glu 715
	Phe Leu Cys Met Lys 720	
Val 725	Leu Leu Leu Leu 725	Asn Thr Ile Pro 730
	Glu Gly Leu Arg Ser 735	Gln
Thr 740	Gln Phe Glu 740	Glu Met Arg Ser 745
	Tyr Ile Arg Glu 750	Leu Ile Lys
Ala 755	Ile Gly 755	Leu Arg Gln Lys 760
	Val Val Ser Ser 765	Gln Arg Phe
Tyr 770	Gln Leu Thr Lys Leu 775	Asp Asn Leu His 780
	Leu Val Lys Gln	
Leu 785	His Leu Tyr Cys Leu 790	Asn Thr Phe Ile 795
	Gln Ser Arg Ala Leu Ser 800	
Val 805	Glu Phe Pro Glu 805	Met Met Ser Glu 810
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	Lys Lys	

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35 40 45

Ser Ala Ile Pro Ile Ser Leu Asp Gly Leu Leu Phe Pro Arg Pro Cys
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Gln Gly Gln Asp Pro Ser Asp Glu Lys Thr Gln Asp Gln Gln Ser Leu
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Ser Asp Val Glu Gly Ala Tyr Ser Arg Ala Glu Ala Thr Arg Gly Ala
85 90 95

Gly Gly Ser Ser Ser Ser Pro Pro Glu Lys Asp Ser Gly Leu Leu Asp
100 105 110

Ser Val Leu Asp Thr Leu Leu Ala Pro Ser Gly Pro Gly Gln Ser Gln
115 120 125

Pro Ser Pro Pro Ala Cys Glu Val Thr Ser Ser Trp Cys Leu Phe Gly
130 135 140

Pro Glu Leu Pro Glu Asp Pro Pro Ala Ala Pro Ala Thr Gln Arg Val
145 150 155 160

Leu Ser Pro Leu Met Ser Arg Ser Gly Cys Lys Val Gly Asp Ser Ser
165 170 175

Gly Thr Ala Ala Ala His Lys Val Leu Pro Arg Gly Leu Ser Pro Ala
180 185 190

Arg Gln Leu Leu Leu Pro Ala Ser Glu Ser Pro His Trp Ser Gly Ala
195 200 205

Pro Val Lys Pro Ser Pro Gln Ala Ala Ala Val Glu Val Glu Glu Glu
210 215 220

Asp Gly Ser Glu Ser Glu Glu Ser Ala Gly Pro Leu Leu Lys Gly Lys
225 230 235 240

Pro Arg Ala Leu Gly Gly Ala Ala Ala Gly Gly Gly Ala Ala Ala Val
245 250 255

Pro Pro Gly Ala Ala Ala Gly Gly Val Ala Leu Val Pro Lys Glu Asp
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 His Val Pro Ile Leu Pro Leu Asn His Ala Leu Leu Ala Ala Arg Thr
 305 310 315 320
 Arg Gln Leu Leu Glu Asp Glu Ser Tyr Asp Gly Gly Ala Gly Ala Ala
 325 330 335
 Ser Ala Phe Ala Pro Pro Arg Ser Ser Pro Cys Ala Ser Ser Thr Pro
 340 345 350
 Val Ala Val Gly Asp Phe Pro Asp Cys Ala Tyr Pro Pro Asp Ala Glu
 355 360 365
 Pro Lys Asp Asp Ala Tyr Pro Leu Tyr Ser Asp Phe Gln Pro Pro Ala
 370 375 380
 Leu Lys Ile Lys Glu Glu Glu Glu Gly Ala Glu Ala Ser Ala Arg Ser
 385 390 395 400
 Pro Arg Ser Tyr Leu Val Ala Gly Ala Asn Pro Ala Ala Phe Pro Asp
 405 410 415
 Phe Pro Leu Gly Pro Pro Pro Pro Leu Pro Pro Arg Ala Thr Pro Ser
 420 425 430
 Arg Pro Gly Glu Ala Ala Val Thr Ala Ala Pro Ala Ser Ala Ser Val
 435 440 445
 Ser Ser Ala Ser Ser Ser Gly Ser Thr Leu Glu Cys Ile Leu Tyr Lys
 450 455 460
 Ala Glu Gly Ala Pro Pro Gln Gln Gly Pro Phe Ala Pro Pro Pro Cys
 465 470 475 480
 Lys Ala Pro Gly Ala Ser Gly Cys Leu Leu Pro Arg Asp Gly Leu Pro
 485 490 495
 Ser Thr Ser Ala Ser Ala Ala Ala Ala Gly Ala Ala Pro Ala Leu Tyr
 500 505 510

Pro Ala Leu Gly Leu Asn Gly Leu Pro Gln Leu Gly Tyr Gln Ala Ala
515 520 525

Val Leu Lys Glu Gly Leu Pro Gln Val Tyr Pro Pro Tyr Leu Asn Tyr
530 535 540

Leu Arg Pro Asp Ser Glu Ala Ser Gln Ser Pro Gln Tyr Ser Phe Glu
545 550 555 560

Ser Leu Pro Gln Lys Ile Cys Leu Ile Cys Gly Asp Glu Ala Ser Gly
565 570 575

Cys His Tyr Gly Val Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Lys
580 585 590

Arg Ala Met Glu Gly Gln His Asn Tyr Leu Cys Ala Gly Arg Asn Asp
595 600 605

Cys Ile Val Asp Lys Ile Arg Arg Lys Asn Cys Pro Ala Cys Arg Leu
610 615 620

Arg Lys Cys Cys Gln Ala Gly Met Val Leu Gly Gly Phe Arg Asn Leu
625 630 635 640

His Ile Asp Asp Gln Ile Thr Leu Ile Gln Tyr Ser Trp Met Ser Leu
645 650 655

Met Val Phe Gly Leu Gly Trp Arg Ser Tyr Lys His Val Ser Gly Gln
660 665 670

Met Leu Tyr Phe Ala Pro Asp Leu Ile Leu Asn Asp Ser Phe Gly Arg
675 680 685

Ala Thr Lys Ser Asn Pro Val
690 695

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<309> 2004-09-03
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Gly Pro Pro Ser Pro Glu Val Gly Ser Pro Leu Leu Cys Arg Pro Ala

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		35					40					45			
Ser	Ala	Ile	Pro	Ile	Ser	Leu	Asp	Gly	Leu	Leu	Phe	Pro	Arg	Pro	Cys
	50					55					60				
Gln	Gly	Gln	Asp	Pro	Ser	Asp	Glu	Lys	Thr	Gln	Asp	Gln	Gln	Ser	Leu
65					70					75					80
Ser	Asp	Val	Glu	Gly	Ala	Tyr	Ser	Arg	Ala	Glu	Ala	Thr	Arg	Gly	Ala
				85					90					95	
Gly	Gly	Ser	Ser	Ser	Pro	Pro	Glu	Lys	Asp	Ser	Gly	Leu	Leu	Asp	
			100				105					110			
Ser	Val	Leu	Asp	Thr	Leu	Leu	Ala	Pro	Ser	Gly	Pro	Gly	Gln	Ser	Gln
		115					120					125			
Pro	Ser	Pro	Pro	Ala	Cys	Glu	Val	Thr	Ser	Ser	Trp	Cys	Leu	Phe	Gly
	130					135					140				
Pro	Glu	Leu	Pro	Glu	Asp	Pro	Pro	Ala	Ala	Pro	Ala	Thr	Gln	Arg	Val
145					150					155					160
Leu	Ser	Pro	Leu	Met	Ser	Arg	Ser	Gly	Cys	Lys	Val	Gly	Asp	Ser	Ser
				165					170					175	
Gly	Thr	Ala	Ala	Ala	His	Lys	Val	Leu	Pro	Arg	Gly	Leu	Ser	Pro	Ala
			180					185					190		
Arg	Gln	Leu	Leu	Leu	Pro	Ala	Ser	Glu	Ser	Pro	His	Trp	Ser	Gly	Ala
		195					200					205			
Pro	Val	Lys	Pro	Ser	Pro	Gln	Ala	Ala	Ala	Val	Glu	Val	Glu	Glu	Glu
	210					215					220				
Asp	Gly	Ser	Glu	Ser	Glu	Glu	Ser	Ala	Gly	Pro	Leu	Leu	Lys	Gly	Lys
225					230					235					240
Pro	Arg	Ala	Leu	Gly	Gly	Ala	Ala	Ala	Gly	Gly	Gly	Ala	Ala	Ala	Val
				245					250					255	
Pro	Pro	Gly	Ala	Ala	Ala	Gly	Gly	Val	Ala	Leu	Val	Pro	Lys	Glu	Asp
			260					265					270		
Ser	Arg	Phe	Ser	Ala	Pro	Arg	Val	Ala	Leu	Val	Glu	Gln	Asp	Ala	Pro
		275					280					285			

Met Ala Pro Gly Arg Ser Pro Leu Ala Thr Thr Val Met Asp Phe Ile
 290 295 300
 His Val Pro Ile Leu Pro Leu Asn His Ala Leu Leu Ala Ala Arg Thr
 305 310 315 320
 Arg Gln Leu Leu Glu Asp Glu Ser Tyr Asp Gly Gly Ala Gly Ala Ala
 325 330 335
 Ser Ala Phe Ala Pro Pro Arg Ser Ser Pro Cys Ala Ser Ser Thr Pro
 340 345 350
 Val Ala Val Gly Asp Phe Pro Asp Cys Ala Tyr Pro Pro Asp Ala Glu
 355 360 365
 Pro Lys Asp Asp Ala Tyr Pro Leu Tyr Ser Asp Phe Gln Pro Pro Ala
 370 375 380
 Leu Lys Ile Lys Glu Glu Glu Glu Gly Ala Glu Ala Ser Ala Arg Ser
 385 390 395 400
 Pro Arg Ser Tyr Leu Val Ala Gly Ala Asn Pro Ala Ala Phe Pro Asp
 405 410 415
 Phe Pro Leu Gly Pro Pro Pro Pro Leu Pro Pro Arg Ala Thr Pro Ser
 420 425 430
 Arg Pro Gly Glu Ala Ala Val Thr Ala Ala Pro Ala Ser Ala Ser Val
 435 440 445
 Ser Ser Ala Ser Ser Ser Gly Ser Thr Leu Glu Cys Ile Leu Tyr Lys
 450 455 460
 Ala Glu Gly Ala Pro Pro Gln Gln Gly Pro Phe Ala Pro Pro Pro Cys
 465 470 475 480
 Lys Ala Pro Gly Ala Ser Gly Cys Leu Leu Pro Arg Asp Gly Leu Pro
 485 490 495
 Ser Thr Ser Ala Ser Ala Ala Ala Ala Gly Ala Ala Pro Ala Leu Tyr
 500 505 510
 Pro Ala Leu Gly Leu Asn Gly Leu Pro Gln Leu Gly Tyr Gln Ala Ala
 515 520 525
 Val Leu Lys Glu Gly Leu Pro Gln Val Tyr Pro Pro Tyr Leu Asn Tyr
 530 535 540

Leu Arg Pro Asp Ser Glu Ala Ser Gln Ser Pro Gln Tyr Ser Phe Glu
 545 550 555 560
 Ser Leu Pro Gln Lys Ile Cys Leu Ile Cys Gly Asp Glu Ala Ser Gly
 565 570 575
 Cys His Tyr Gly Val Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Lys
 580 585 590
 Arg Ala Met Glu Gly Arg Lys Phe Lys Lys Phe Asn Lys Val Arg Val
 595 600 605
 Val Arg Ala Leu Asp Ala Val Ala Leu Pro Gln Pro Val Gly Val Pro
 610 615 620
 Asn Glu Ser Gln Ala Leu Ser Gln Arg Phe Thr Phe Ser Pro Gly Gln
 625 630 635 640
 Asp Ile Gln Leu Ile Pro Pro Leu Ile Asn Leu Leu Met Ser Ile Glu
 645 650 655
 Pro Asp Val Ile Tyr Ala Gly His Asp Asn Thr Lys Pro Asp Thr Ser
 660 665 670
 Ser Ser Leu Leu Thr Ser Leu Asn Gln Leu Gly Glu Arg Gln Leu Leu
 675 680 685
 Ser Val Val Lys Trp Ser Lys Ser Leu Pro Gly Phe Arg Asn Leu His
 690 695 700
 Ile Asp Asp Gln Ile Thr Leu Ile Gln Tyr Ser Trp Met Ser Leu Met
 705 710 715 720
 Val Phe Gly Leu Gly Trp Arg Ser Tyr Lys His Val Ser Gly Gln Met
 725 730 735
 Leu Tyr Phe Ala Pro Asp Leu Ile Leu Asn Glu Ser His Arg Ser Leu
 740 745 750
 Ser Ser Phe Lys Leu Ala Lys Lys Ser Ser Ser Val
 755 760

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Gly Pro Pro Ser Pro Glu Val Gly Ser Pro Leu Leu Cys Arg Pro Ala
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Ala Gly Pro Phe Pro Gly Ser Gln Thr Ser Asp Thr Leu Pro Glu Val
35 40 45

Ser Ala Ile Pro Ile Ser Leu Asp Gly Leu Leu Phe Pro Arg Pro Cys
50 55 60

Gln Gly Gln Asp Pro Ser Asp Glu Lys Thr Gln Asp Gln Gln Ser Leu
65 70 75 80

Ser Asp Val Glu Gly Ala Tyr Ser Arg Ala Glu Ala Thr Arg Gly Ala
85 90 95

Gly Gly Ser Ser Ser Ser Pro Pro Glu Lys Asp Ser Gly Leu Leu Asp
100 105 110

Ser Val Leu Asp Thr Leu Leu Ala Pro Ser Gly Pro Gly Gln Ser Gln
115 120 125

Pro Ser Pro Pro Ala Cys Glu Val Thr Ser Ser Trp Cys Leu Phe Gly
130 135 140

Pro Glu Leu Pro Glu Asp Pro Pro Ala Ala Pro Ala Thr Gln Arg Val
145 150 155 160

Leu Ser Pro Leu Met Ser Arg Ser Gly Cys Lys Val Gly Asp Ser Ser
165 170 175

Gly Thr Ala Ala Ala His Lys Val Leu Pro Arg Gly Leu Ser Pro Ala
180 185 190

Arg Gln Leu Leu Leu Pro Ala Ser Glu Ser Pro His Trp Ser Gly Ala
195 200 205

Pro Val Lys Pro Ser Pro Gln Ala Ala Ala Val Glu Val Glu Glu Glu
210 215 220

Asp Gly Ser Glu Ser Glu Glu Ser Ala Gly Pro Leu Leu Lys Gly Lys
225 230 235 240

Pro Arg Ala Leu Gly Gly Ala Ala Ala Gly Gly Gly Ala Ala Ala Val

245										250					255				
Pro	Pro	Gly	Ala 260	Ala	Ala	Gly	Gly	Val 265	Ala	Leu	Val	Pro	Lys 270	Glu	Asp				
Ser	Arg	Phe 275	Ser	Ala	Pro	Arg	Val 280	Ala	Leu	Val	Glu	Gln 285	Asp	Ala	Pro				
Met	Ala 290	Pro	Gly	Arg	Ser	Pro 295	Leu	Ala	Thr	Thr	Val 300	Met	Asp	Phe	Ile				
His 305	Val	Pro	Ile	Leu	Pro 310	Leu	Asn	His	Ala	Leu 315	Leu	Ala	Ala	Arg	Thr 320				
Arg	Gln	Leu	Leu	Glu 325	Asp	Glu	Ser	Tyr	Asp 330	Gly	Gly	Ala	Gly	Ala 335	Ala				
Ser	Ala	Phe	Ala 340	Pro	Pro	Arg	Ser	Ser 345	Pro	Cys	Ala	Ser	Ser 350	Thr	Pro				
Val	Ala	Val 355	Gly	Asp	Phe	Pro	Asp 360	Cys	Ala	Tyr	Pro	Pro 365	Asp	Ala	Glu				
Pro	Lys 370	Asp	Asp	Ala	Tyr	Pro 375	Leu	Tyr	Ser	Asp	Phe 380	Gln	Pro	Pro	Ala				
Leu 385	Lys	Ile	Lys	Glu	Glu 390	Glu	Glu	Gly	Ala	Glu 395	Ala	Ser	Ala	Arg	Ser 400				
Pro	Arg	Ser	Tyr	Leu 405	Val	Ala	Gly	Ala	Asn 410	Pro	Ala	Ala	Phe	Pro 415	Asp				
Phe	Pro	Leu	Gly 420	Pro	Pro	Pro	Pro	Leu 425	Pro	Pro	Arg	Ala	Thr 430	Pro	Ser				
Arg	Pro	Gly 435	Glu	Ala	Ala	Val	Thr 440	Ala	Ala	Pro	Ala	Ser 445	Ala	Ser	Val				
Ser	Ser 450	Ala	Ser	Ser	Ser	Gly 455	Ser	Thr	Leu	Glu	Cys 460	Ile	Leu	Tyr	Lys				
Ala 465	Glu	Gly	Ala	Pro	Pro 470	Gln	Gln	Gly	Pro	Phe 475	Ala	Pro	Pro	Pro	Cys 480				
Lys	Ala	Pro	Gly	Ala 485	Ser	Gly	Cys	Leu	Leu 490	Pro	Arg	Asp	Gly	Leu 495	Pro				
Ser	Thr	Ser	Ala 500	Ser	Ala	Ala	Ala	Ala 505	Gly	Ala	Ala	Pro	Ala 510	Leu	Tyr				

Pro Ala Leu Gly Leu Asn Gly Leu Pro Gln Leu Gly Tyr Gln Ala Ala
515 520 525

Val Leu Lys Glu Gly Leu Pro Gln Val Tyr Pro Pro Tyr Leu Asn Tyr
530 535 540

Leu Arg Pro Asp Ser Glu Ala Ser Gln Ser Pro Gln Tyr Ser Phe Glu
545 550 555 560

Ser Leu Pro Gln Lys Ile Cys Leu Ile Cys Gly Asp Glu Ala Ser Gly
565 570 575

Cys His Tyr Gly Val Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Lys
580 585 590

Arg Ala Met Glu Gly Gln His Asn Tyr Leu Cys Ala Gly Arg Asn Asp
595 600 605

Cys Ile Val Asp Lys Ile Arg Arg Lys Asn Cys Pro Ala Cys Arg Leu
610 615 620

Arg Lys Cys Cys Gln Ala Gly Met Val Leu Gly Gly Phe Arg Asn Leu
625 630 635 640

His Ile Asp Asp Gln Ile Thr Leu Ile Gln Tyr Ser Trp Met Ser Leu
645 650 655

Met Val Phe Gly Leu Gly Trp Arg Ser Tyr Lys His Val Ser Gly Gln
660 665 670

Met Leu Tyr Phe Ala Pro Asp Leu Ile Leu Asn Glu Gln Ser Ile Val
675 680 685

Thr Ser
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Gly Pro Pro Ser₂₀ Pro Glu Val Gly Ser₂₅ Pro Leu Leu Cys Arg₃₀ Pro Ala
 Ala Gly Pro₃₅ Phe Pro Gly Ser₄₀ Gln Thr Ser Asp Thr Leu₄₅ Pro Glu Val
 Ser Ala₅₀ Ile Pro Ile Ser₅₅ Leu Asp Gly Leu Leu Phe₆₀ Pro Arg Pro Cys
 Gln Gly Gln Asp Pro Ser₇₀ Asp Glu Lys Thr Gln₇₅ Asp Gln Gln Ser Leu₈₀
 Ser Asp Val Glu₈₅ Gly Ala Tyr Ser Arg Ala₉₀ Glu Ala Thr Arg Gly₉₅ Ala
 Gly Gly Ser₁₀₀ Ser Ser Pro Pro Glu₁₀₅ Lys Asp Ser Gly Leu₁₁₀ Leu Asp
 Ser Val Leu₁₁₅ Asp Thr Leu Leu Ala₁₂₀ Pro Ser Gly Pro Gly₁₂₅ Gln Ser Gln
 Pro Ser₁₃₀ Pro Pro Ala Cys Glu₁₃₅ Val Thr Ser Ser Trp₁₄₀ Cys Leu Phe Gly
 Pro Glu Leu Pro Glu Asp₁₅₀ Pro Pro Ala Ala Pro₁₅₅ Ala Thr Gln Arg Val₁₆₀
 Leu Ser Pro Leu Met₁₆₅ Ser Arg Ser Gly Cys₁₇₀ Lys Val Gly Asp Ser₁₇₅ Ser
 Gly Thr Ala Ala₁₈₀ Ala His Lys Val Leu₁₈₅ Pro Arg Gly Leu Ser₁₉₀ Pro Ala
 Arg Gln Leu₁₉₅ Leu Leu Pro Ala Ser₂₀₀ Glu Ser Pro His Trp₂₀₅ Ser Gly Ala
 Pro Val₂₁₀ Lys Pro Ser Pro Gln₂₁₅ Ala Ala Ala Val Glu₂₂₀ Val Glu Glu Glu
 Asp Gly Ser Glu Ser Glu₂₃₀ Glu Ser Ala Gly Pro₂₃₅ Leu Leu Lys Gly Lys₂₄₀
 Pro Arg Ala Leu Gly₂₄₅ Gly Ala Ala Ala Gly₂₅₀ Gly Gly Ala Ala Ala Val₂₅₅
 Pro Pro Gly Ala₂₆₀ Ala Ala Gly Gly Val₂₆₅ Ala Leu Val Pro Lys₂₇₀ Glu Asp

Ser Arg Phe Ser Ala Pro Arg Val Ala Leu Val Glu Gln Asp Ala Pro
 275 280 285
 Met Ala Pro Gly Arg Ser Pro Leu Ala Thr Thr Val Met Asp Phe Ile
 290 295 300
 His Val Pro Ile Leu Pro Leu Asn His Ala Leu Leu Ala Ala Arg Thr
 305 310 315 320
 Arg Gln Leu Leu Glu Asp Glu Ser Tyr Asp Gly Gly Ala Gly Ala Ala
 325 330 335
 Ser Ala Phe Ala Pro Pro Arg Ser Ser Pro Cys Ala Ser Ser Thr Pro
 340 345 350
 Val Ala Val Gly Asp Phe Pro Asp Cys Ala Tyr Pro Pro Asp Ala Glu
 355 360 365
 Pro Lys Asp Asp Ala Tyr Pro Leu Tyr Ser Asp Phe Gln Pro Pro Ala
 370 375 380
 Leu Lys Ile Lys Glu Glu Glu Glu Gly Ala Glu Ala Ser Ala Arg Ser
 385 390 395 400
 Pro Arg Ser Tyr Leu Val Ala Gly Ala Asn Pro Ala Ala Phe Pro Asp
 405 410 415
 Phe Pro Leu Gly Pro Pro Pro Pro Leu Pro Pro Arg Ala Thr Pro Ser
 420 425 430
 Arg Pro Gly Glu Ala Ala Val Thr Ala Ala Pro Ala Ser Ala Ser Val
 435 440 445
 Ser Ser Ala Ser Ser Ser Gly Ser Thr Leu Glu Cys Ile Leu Tyr Lys
 450 455 460
 Ala Glu Gly Ala Pro Pro Gln Gln Gly Pro Phe Ala Pro Pro Pro Cys
 465 470 475 480
 Lys Ala Pro Gly Ala Ser Gly Cys Leu Leu Pro Arg Asp Gly Leu Pro
 485 490 495
 Ser Thr Ser Ala Ser Ala Ala Ala Ala Gly Ala Ala Pro Ala Leu Tyr
 500 505 510
 Pro Ala Leu Gly Leu Asn Gly Leu Pro Gln Leu Gly Tyr Gln Ala Ala
 515 520 525
 Val Leu Lys Glu Gly Leu Pro Gln Val Tyr Pro Pro Tyr Leu Asn Tyr

530					535					540					
Leu 545	Arg	Pro	Asp	Ser	Glu 550	Ala	Ser	Gln	Ser	Pro 555	Gln	Tyr	Ser	Phe	Glu 560
Ser	Leu	Pro	Gln	Lys 565	Ile	Cys	Leu	Ile	Cys 570	Gly	Asp	Glu	Ala	Ser	Gly 575
Cys	His	Tyr	Gly 580	Val	Leu	Thr	Cys	Gly 585	Ser	Cys	Lys	Val	Phe 590	Phe	Lys
Arg	Ala	Met 595	Glu	Gly	Gln	His	Asn 600	Tyr	Leu	Cys	Ala	Gly 605	Arg	Asn	Asp
Cys	Ile 610	Val	Asp	Lys	Ile	Arg 615	Arg	Lys	Asn	Cys	Pro 620	Ala	Cys	Arg	Leu
Arg 625	Lys	Cys	Cys	Gln	Ala 630	Gly	Met	Val	Leu	Gly 635	Gly	Arg	Lys	Phe	Lys 640
Lys	Phe	Asn	Lys	Val 645	Arg	Val	Val	Arg	Ala 650	Leu	Asp	Ala	Val	Ala 655	Leu
Pro	Gln	Pro	Val 660	Gly	Val	Pro	Asn	Glu 665	Ser	Gln	Ala	Leu	Ser 670	Gln	Arg
Phe	Thr	Phe 675	Ser	Pro	Gly	Gln	Asp 680	Ile	Gln	Leu	Ile	Pro 685	Pro	Leu	Ile
Asn 690	Leu	Leu	Met	Ser	Ile	Glu 695	Pro	Asp	Val	Ile	Tyr 700	Ala	Gly	His	Asp
Asn 705	Thr	Lys	Pro	Asp	Thr 710	Ser	Ser	Ser	Leu	Leu 715	Thr	Ser	Leu	Asn	Gln 720
Leu	Gly	Glu	Arg	Gln 725	Leu	Leu	Ser	Val	Val 730	Lys	Trp	Ser	Lys	Ser 735	Leu
Pro	Gly	Phe	Arg 740	Asn	Leu	His	Ile	Asp 745	Asp	Gln	Ile	Thr	Leu 750	Ile	Gln
Tyr	Ser	Trp 755	Met	Ser	Leu	Met	Val 760	Phe	Gly	Leu	Gly	Trp 765	Arg	Ser	Tyr
Lys	His 770	Val	Ser	Gly	Gln	Met 775	Leu	Tyr	Phe	Ala	Pro 780	Asp	Leu	Ile	Leu
Asn 785	Glu	Ser	His	Arg	Ser 790	Leu	Ser	Ser	Phe	Lys 795	Leu	Ala	Lys	Lys	Ser 800

Ser Ser Val

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<400> 16

Phe Gly Gln Gly Gly Ala Gly Pro Val Gly Gly Gln Gly Pro
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<400> 17
ctgagtc

7

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Tyr Gly Glu Pro Gly Glu Val Phe Ile Asn Lys Gly Lys
1 5 10

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Gly Ile Val Glu Phe Ala Ser Lys Pro Ala Ala Arg
1 5 10

<210> 20
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<213> Homo sapiens

<400> 20

Phe Ala Gln His Gly Thr Glu Glu Tyr Glu Tyr Ser Gln Arg
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<309> 2004-08-24
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Met Ser Arg Asp Arg Phe Arg Ser Arg Gly Gly Gly Gly Gly Gly Phe
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His Arg Arg Gly Gly Gly Gly Gly Arg Gly Gly Leu His Asp Phe Arg
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Ser Pro Pro Pro Gly Met Gly Leu Asn Gln Asn Arg Gly Pro Met Gly
35 40 45

Pro Gly Pro Gly Gly Pro Lys Pro Pro Leu Pro Pro Pro Pro His
50 55 60

Gln Gln Gln Gln Gln Pro Pro Pro Gln Gln Pro Pro Gln Gln Pro
65 70 75 80

Pro Pro His Gln Gln Pro Pro Pro His Gln Pro Pro His Gln Gln Pro
85 90 95

Pro Pro Pro Pro Gln Glu Ser Lys Pro Val Val Pro Gln Gly Pro Gly
100 105 110

Ser Ala Pro Gly Val Ser Ser Ala Pro Pro Pro Ala Val Ser Ala Pro
115 120 125

Pro Ala Asn Pro Pro Thr Thr Gly Ala Pro Pro Gly Pro Gly Pro Thr
130 135 140

Pro Thr Pro Pro Pro Ala Val Pro Ser Thr Ala Pro Gly Pro Pro Pro
145 150 155 160

Pro Ser Thr Pro Ser Ser Gly Val Ser Thr Thr Pro Pro Gln Thr Gly
165 170 175

Gly Pro Pro Pro Pro Pro Ala Gly Gly Ala Gly Pro Gly Pro Lys Pro
180 185 190

Gly Pro Gly Pro Gly Gly Pro Lys Gly Gly Lys Met Pro Gly Gly Pro
195 200 205

Lys Pro Gly Gly Gly Pro Gly Met Gly Ala Pro Gly Gly His Pro Lys
210 215 220

Pro Pro His Arg Gly Gly Gly Glu Pro Arg Gly Gly Arg Gln His His
225 230 235 240

Ala Pro Tyr His Gln Gln His His Gln Gly Pro Pro Pro Gly Gly Pro
 245 250 255
 Gly Pro Arg Thr Glu Glu Lys Ile Ser Asp Ser Glu Gly Phe Lys Ala
 260 265 270
 Asn Leu Ser Leu Leu Arg Arg Pro Gly Glu Lys Thr Tyr Thr Gln Arg
 275 280 285
 Cys Arg Leu Phe Val Gly Asn Leu Pro Ala Asp Ile Thr Glu Asp Glu
 290 295 300
 Phe Lys Arg Leu Phe Ala Lys Tyr Gly Glu Pro Gly Glu Val Phe Ile
 305 310 315 320
 Asn Lys Gly Lys Gly Phe Gly Phe Ile Lys Leu Glu Ser Arg Ala Leu
 325 330 335
 Ala Glu Ile Ala Lys Ala Glu Leu Asp Asp Thr Pro Met Arg Gly Arg
 340 345 350
 Gln Leu Arg Val Arg Phe Ala Thr His Ala Ala Ala Leu Ser Val Arg
 355 360 365
 Asn Leu Ser Pro Tyr Val Ser Asn Glu Leu Leu Glu Glu Ala Phe Ser
 370 375 380
 Gln Phe Gly Pro Ile Glu Arg Ala Val Val Ile Val Asp Asp Arg Gly
 385 390 395 400
 Arg Ser Thr Gly Lys Gly Ile Val Glu Phe Ala Ser Lys Pro Ala Ala
 405 410 415
 Arg Lys Ala Phe Glu Arg Cys Ser Glu Gly Val Phe Leu Leu Thr Thr
 420 425 430
 Thr Pro Arg Pro Val Ile Val Glu Pro Leu Glu Gln Leu Asp Asp Glu
 435 440 445
 Asp Gly Leu Pro Glu Lys Leu Ala Gln Lys Asn Pro Met Tyr Gln Lys
 450 455 460
 Glu Arg Glu Thr Pro Pro Arg Phe Ala Gln His Gly Thr Phe Glu Tyr
 465 470 475 480
 Glu Tyr Ser Gln Arg Trp Lys Ser Leu Asp Glu Met Glu Lys Gln Gln
 485 490 495

Arg Glu Gln Val Glu Lys Asn Met Lys Asp Ala Lys Asp Lys Leu Glu
 500 505 510
 Ser Glu Met Glu Asp Ala Tyr His Glu His Gln Ala Asn Leu Leu Arg
 515 520 525
 Gln Asp Leu Met Arg Arg Gln Glu Glu Leu Arg Arg Met Glu Glu Leu
 530 535 540
 His Ser Gln Glu Met Gln Lys Arg Lys Glu Met Gln Leu Arg Gln Glu
 545 550 555 560
 Glu Glu Arg Arg Arg Arg Glu Glu Glu Met Met Ile Arg Gln Arg Glu
 565 570 575
 Met Glu Glu Gln Met Arg Arg Gln Arg Glu Glu Ser Tyr Ser Arg Met
 580 585 590
 Gly Tyr Met Asp Pro Arg Glu Arg Asp Met Arg Met Gly Gly Gly Gly
 595 600 605
 Thr Met Asn Met Gly Asp Pro Tyr Gly Ser Gly Gly Gln Lys Phe Pro
 610 615 620
 Pro Leu Gly Gly Gly Gly Gly Ile Gly Tyr Glu Ala Asn Pro Gly Val
 625 630 635 640
 Pro Pro Ala Thr Met Ser Gly Ser Met Met Gly Ser Asp Met Arg Thr
 645 650 655
 Glu Arg Phe Gly Gln Gly Gly Ala Gly Pro Val Gly Gly Gln Gly Pro
 660 665 670
 Arg Gly Met Gly Pro Gly Thr Pro Ala Gly Tyr Gly Arg Gly Arg Glu
 675 680 685
 Glu Tyr Glu Gly Pro Asn Lys Lys Pro Arg Phe
 690 695

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 <212> PRT
 <213> Homo sapiens

<400> 22

Val Arg Met Ile Asp Val Gly
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Sequence Listing

SEQ ID NO. 1

5 PSF Long Form PSF-A

P23246

707 aa linear

10 Splicing factor, proline-and glutamine-rich (Polypyrimidine tract-binding protein-associated splicing factor) (PTB-associated splicing factor) (PSF) (DNA-binding p52/p100 complex, 100 kDa subunit).

NP_005057

15 splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated) [Homo sapiens].

CAA50283

707 aa linear

20 PTB-associated splicing factor [Homo sapiens].

1 msrdrfrsrg gggggfhrrg ggggrgglhd frspppgmgl nqnrpgmgrp pgqsgpkppi
61 ppppphqqqq qpppqpppp qppphqppph ppphqqqqpp pppqdsskpv vaqgpgpapg
121 vgsappasss appatpptsq appgsgpgpt ptpppavtsa ppgappptpp ssgvpttppq
181 agggppppaa vpgpgpgpkq gpgpgpgkqg kmpggpkpgg gpglstpggh pkpphrggge
25 241 prggrqhphp yhqqhghgpp pggpggrsee kisdsegfka nlsllrrpge ktytqrclrf
301 vgnlpadite defkrlfaky gepgevfink gkgfgfikle sralaeiaka elddtpmrgr
361 qlrvrfatha aalsvrnlsp yvsnelleea fsqfgpiera vvivddrgs tgkgivefas
421 kpaarkafer csegvfltt tprpvivepl eqlddedglp eklaqknpm qkeretpprf
481 aqhgtfeyey sqrwksldem ekqgrequek nmkdakdkle semedayheh qanllrqdlm
30 541 rrqeelrme elhnqemqkr kemqlrquee rrrreeemmi rgreemeeqr rgreesyarm
601 gymdprerdm rmggggamnm gdpysgggqk fpplgggggi gyeangvpp atmsgsmmgs
661 dmrterfggg gagpvgggpp rgmgpgtpag ygrgreeyeg pnkkprf

35 SEQ ID NO. 2

AAH51192

707 aa linear

40 Splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated) [Homo sapiens].

1 msrdrfrsrg gggggfhrrg ggggrgglhd frspppgmgl nqnrpgmgrp pgqsgpkppi
61 ppppphqqqq qpppqpppp qppphqppph ppphqqqqpp pppqdsskpv vaqgpgpapg
121 vgstppasss appatpptsq appgsgpgpt ptpppavtsa ppgappptpp ssgvpttppq
45 181 agggppppaa vpgpgpgpkq gpgpgpgkqg kmpggpkpgg gpglstpggh pkpprrggge
241 prggrqhphp yhqqhghgpp pggpggrsee kisdsegfka nlsllrrpge ktytqrclrf
301 vgnlpadite defkrlfaky gepgevfink gkgfgfikle sralaeiaka elddtpmrgr
361 qlrvrfatha aalsvrnlsp yvsnelleea fsqfgpiera vvivddrgs tgkgivefas
421 kpaarkafer csegvfltt tprpvivepl eqlddedglp eklaqknpm qkeretptrf
50 481 aqhgtfeyey sqrwksldem ekqgrequek nmkdakdkle semedayheh qanllrqdlm
541 rrqeelrme elhnqemqkr kemqlrquee rrrreeemmi rgreemeeqr rgreesyarm
601 gymdprerdm rmggggamnm gdpysgggqk fpplgggggi gyeangvpp atmsgsmmgs
661 dmrterfggg gagpvgggpp rgmgpgtpag ygrgreeyeg pnkkprf

55

SEQ ID NO. 3

Isoform short - PSF-F
569aa

5
1 msrdfrfrsrg gggggfhrhg ggggrggldh frspppgmg1 nqnrpgmpgpg pgqsgpkppi
61 ppppphqqqq qpppqpppq qppphqppph ppphqqqqpp pppqdsskpva qagpgpapg
121 vgsappasss appatppts appgsgpgpt ptpppavtsa ppgappptpp ssgvpttppq
181 agggppppaa vpgpgpgpkq gpgpgpgkgg kmpggpkpgg gpglstpggh pkpphrggge
10 241 prggrqhphp yhqghhgpp gggpggrsee kisdsegfka nlsllrrpge ktytqrcrlf
301 vgnlpadite defkrlfaky gepgevfink gkgfgfikle sralaeiaka elddtpmrgr
361 qlrvrfatha aalsvrnlsp yvsnelleea fsqfgpiera vvivddrgrs tgkgivefas
421 kpaarkafer csegvlltt tprpvivepl eqlddedglp eklagknpm yqkeretpprf
481 aqhgtfeyey sqrwksldem ekqgreveq nmkdakdkle semedayheh qanllrqdlm
15 541 rrqeelrrme elhngemqkr kemqlrquee rrrreeemmi rremeeqmr rgreesysrm
601 gymdprerdm rmggggamnm gdpysgggk fpplgggggi gyeangpvpp atmaggmmgs
661 dmvrmidvg

20 SEQ ID NO. 4

AAH04534
634 aa linear
SFPQ protein [Homo sapiens].

25
1 pqqppppqqpp phqppphpp hqqqqppppp qdsskpvaq gpgpapgvgs appasssapp
61 atpptsagpp gsgpgtptp ppavtsappg appptppssg vpttppqagg pppppaavpg
121 ppgpgkqpgg pggpkggkmp gpgkpgggpg lstpgghpkp phrgggeprg grqhppyhq
181 qhhqgpppgg pgggrseekis dsegfkanls llrrpgeky tqrcrlfvgn lpaditedef
30 241 krlfakygep gevfindkkg fgfiklesra laeiakaeld dtpmrgrqlr vrfathaaal
301 svrnlsyvs nelleeafsq fgpiervvi vddrgrstgk givefaskpa arkafercse
361 gvlltttpr pvivepleql ddedglpekl aqknpm yqkeretpprf
421 wksldemekq greqveknmk dakdklesem edayhehqan llrqdlmrrq eelrrmeelh
481 ngemqkrkem qlrqueerrr reeemmirqr emeeqmrqr eesysrmgym dprerdmrmg
35 541 gggamnmgdp ysgggkfp lggggigye anpgvppatm sgsmmgsdmr terfggggag
601 pvggqgprgm gpgtpagygr greeyegpnk kprf

SEQ ID NO. 5

40
AAH27708
525 aa linear
SFPQ protein [Homo sapiens].

45
1 msrdfrfrsrg gggggfhrhg ggggrggldh frspppgmg1 nqnrpgmpgpg pgqsgpkppi
61 ppppphqqqq qpppqpppq qppphqppph ppphqqqqpp pppqdsskpva qagpgpapg
121 vgsappasss appatppts appgsgpgpt ptpppavtsa ppgappptpp ssgvpttppq
181 agggppppaa vpgpgpgpkq gpgpgpgkgg kmpggpkpgg gpglstpggh pkpphrggge
241 prggrqhphp yhqghhgpp gggpggrsee kisdsegfka nlsllrrpge ktytqrcrlf
50 301 vgnlpadite defkrlfaky gepgevfink gkgfgfikle sralaeiaka elddtpmrgr
361 qlrvrfatha aalsvrnlsp yvsnelleea fsqfgpiera vvivddrgrs tgkgivefas
421 kpaarkafer csegvlltt tprpvivepl eqlddedglp eklagknpm yqkeretpprf
481 aqhgtfeyey sqrwksldem ekqgreveq nmkdakdkl kkkkk

55

SEQ ID. NO. 6

CAA34747

396 aa linear

5 DEFINITION myoblast antigen 24.1D5 (Homo sapiens).

1 efkrlfakyg epgevfvinkg kgfgfikles ralaieiakae lddtpmrgrq lrvrfathaa
61 alsvrnlspy vsnelleeeaf sqfgpierav vivddrgrst gkgivefask paarkaferc
121 segvfltttt prpviveple qlddedglpe klaqknpmq keretpprfa qhgtfeyey
10 181 qrwksldeme kqqreqvekn mkdakdkles emedayhehq anllrqdlmr rqeelrrmee
241 lhnqemqkrk emqlrgeeer rrreeemmir qremeeqmrr greesyarmg ymdprerdmr
301 mgggggammng dpygsggqkf pplggggggig yeapngvppa tmsgsmmgsd mrterfgggg
361 agpvvggggpr gmvgpgrpagy grgreeyegp nkkprf

15

SEQ ID NO. 7

NM_005066

3071 bp mRNA linear

20 Homo sapiens splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated) (SFPQ), mRNA.

X70944 S56626

3071 bp mRNA linear

25 H.sapiens mRNA for PTB-associated splicing factor.

1 ccgccatttt gtgagaagca aggtggcctc cacgtttcct gagcgtcttc ttcgcttttg
61 cctcgaccgc cccttgacca cagacatgtc tcgggatcgg ttccggagtc gtggcgggtg
121 cgggtggtggc ttccacaggc gtggaggagg cggcgggccgc ggcggcctcc acgacttccg
30 181 ttctccgccg ccgggcatgg gcctcaatca gaatcgccgc cccatgggtc ctggcccggg
241 ccagagcggc cctaagcctc cgatcccgc accgcctcca caccaacagc agcaacagcc
301 accaccgcag cagccaccgc cgcagcagcc gccaccgcag cagccgcccgc cgcattccaca
361 gccgcattcag cagcagcagc cgcgcgccacc gccgcaggac tcttccaagc ccgtcgttgc
421 tcagggaccc ggccccgctc ccggagtagg cagcgcacca ccagcctcca gctcggcccc
35 481 gcccgccact ccaccaacct cgggggcccc gccagggtcc gggccaggcc cgactccgac
541 cccgcgcctt gcagtcacct cggccccctc cggggcgccg ccacccaccc cgccaagcag
601 cgggggtcctt accacacctc ctcaggcccg agggccgcgc cctccgcccc cggcagtcctc
661 gggccccgggt ccagggccta agcagggccc aggtccgggt ggtcccaaag gcggcaaat
721 gcctggcggg ccgaagccag gtggcggccc gggcctaagt acgcctggcg gccaccccaa
40 781 gccgcgcgat cgaggcggcg gggagccccg cgggggcccgc cagcaccacc cgccctacca
841 ccagcagcat caccaggggg ccccgcgccg cggggcccgc ggcgcagcg aggagaagat
901 ctcggaactc gaggggttta aagccaattt gtctctcttg aggaggcctg gagagaaac
961 ttacacacag cgatgtcggg tgtttgttgg gaatctacct gctgatatca cggaggatga
1021 attcaaaaga ctatttgcta aatatggaga accaggagaa gtttttatca acaaaggcaa
45 1081 aggattcgga ttatttaagc ttgaatctag agctttggct gaaattgcca aagccgaact
1141 ggatgataca cccatgagag gtagacagct tcgagttcgc tttgccacac atgctgctgc
1201 cctttctgtt cgtaattctt caccttatgt ttccaatgaa ctgttggaag aagcctttag
1261 ccaatttggc cctattgaaa gggctgttgt aatagtggat gatcgtggaa gatctacagg
1321 gaaaggcatt gttgaatttg cttctaagcc agcagcaaga aaggcatttg aacgatgcag
50 1381 tgaagggtgt ttcttactga cgacaactcc tcgtccagtc attgtggaac cacttgaaca
1441 actagatgat gaagatggtc ttcttgaaaa acttgcccag aagaatccaa tgtatcaaaa
1501 ggagagagaa acccctcctc gttttgcccc gcatggcacg tttgagtacg aatattctca
1561 gcgatggaag tctttggatg aaatggaaaa acagcaaagg gaacaagttg aaaaaaacat
1621 gaaagatgca aaagacaaat tggaaagtga aatggaagat gcctatcatg aacatcaggc
55 1681 aaatcttttg cgccaagatc tgatgagacg acaggaagaa ttaagacgca tggaagaact

1741 tcacaatcaa gaaatgcaga aacgtaaaga aatgcaattg aggcaagagg aggaacgacg
1801 tagaagagag gaagagatga tgattcgtca acgtgagatg gaagaacaaa tgaggcgcca
1861 aagagaggaa agttacagcc gaatgggcta catggatcca cgggaaagag acatgcgaat
1921 ggggtggcggg ggagcaatga acatgggaga tccctatggg tcaggaggcc agaaatttcc
5 1981 acctctagga ggtggtggtg gcatagggtt tgaagetaat cctggcggtc caccagcaac
2041 catgagtggg tccatgatgg gaagtgcacat gcgtactgag cgctttgggc agggaggtgc
2101 ggggcctgtg ggtggacagg gtcctagagg aatggggcct ggaactccag caggatatgg
2161 tagagggaga gaagagtacg aaggcccaaa caaaaaaccc cgattttaga tgtgatattt
2221 aggccttcat tccagtttgt tttgtttttt tgtttagata ccaatctttt aaattcttgc
10 2281 attttagtaa gaaagctatc tttttatgga tgtttagcag ttattgacct aatatttgta
2341 aatgggtctgt ttgggcagggt aaaattatgt aatgcagtgt ttggaacagg agaatttttt
2401 tttccttttt atttctttat ttttctttt ttactgtata atgtccctca agtttatggc
2461 agtgtacctt gtgccactga atttccaaag tgtaccaatt tttttttttt tactgtgctt
2521 caaataaata gaaaaatagt tataatattg gatcttcaac tttgccatcc atgcttctat
15 2581 gcatattagg ctacgtatcc cacattgaaa gcatgagagt gtctaggcct ttgaatggca
2641 tatgccattt ctgggaaatg catctggagg ctaagtattg ctttctacaa ataattgcc
2701 cctttgtttt aaaaagaaga aatgcatatt gaagtatgtt gatgatttgt ttggcatata
2761 ggaagcacgc tgggtgctaag tattttttta atggttatgt aagcaaagct gaactgtaaa
2821 tcttcaggaa tatgtattaa gattgtggaa tgggtgtaag acaattggta gggggtgaaa
20 2881 gtgggtttga ttaaattgat cttttatggc cctatgatct atcctttact tgaaagcttt
2941 tgaaaagtgg aaagggtcatt ttgttgcat tccccatttc ttgtttttta aagaccaaca
3001 aatctcaagc cctataaatg gcttgtattg aacttttaca tttgaattaa agatgttaaa
3061 catgaaaaaa a

25

SEQ ID NO. 8

BC051192

2622 bp mRNA linear

30 Homo sapiens splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated), mRNA (cDNA clone), complete cds.

1 tctgtgtcat ccgccatttt gtgagaagca aggtggcctc cacgtttcct gagcgtcttc
61 ttcgcttttg cctcgaccgc cccttgacca cagacatgtc tcgggatcgg ttccggagtc
35 121 gtggcggtgg cgggtggtgg ttccacaggg gtggaggagg cggcgccgcg ggcggcctcc
181 acgacttccg ttctccgccg cccggcatgg gcctcaatca gaatcgcgge cccatgggtc
241 ctggcccggg ccagagcggc cctaagcctc cgatcccgcc accgcctcca caccaacagc
301 agcaacagcc accaccgcag cagccaccgc cgcagcagcc gccaccgcat cagccgcgcg
361 cgcattccaca gccgcatcag cagcagcagc cgcgcgcacc gccgcaggac tcttccaagc
40 421 ccgtcgttgc tcagggaccc ggccccgctc ccggagtagg cagcacacca ccagcctcca
481 gctcggcccc gcccgccact ccaccaacct cgggggcccc gccagggtcc gggccaggcc
541 cgactccgac cccgcgcctt gcagtcacct cggccccctc cggggcgccg ccaccacccc
601 cgccaagcag cgggggtccct accacacctc cttagggcgg agggccgcgg cctccgcccg
661 cggcagtccc gggcccgggt ccagggccta agcaggggcc aggtccgggt ggtcccaaag
45 721 gcggcaaaat gcctggcggg ccgaagccag gtggcggccc gggcctaagt acgcctggcg
781 gccaccccaa gccgcgcgtt cgaggcggcg gggagccccg cgggggcccg cagcaccacc
841 cgccctacca ccagcagcat caccaggggc ccccgcccgg cgggcccggc ggccgcagcg
901 aggagaagat ctccgactcg gaggggttta aagccaattt gtctctcttg aggaggcctg
961 gagagaaaac ttacacacag cgatgtcggg tgtttgttgg gaatctacct gctgatatac
50 1021 cggaggatga attcaaaaga ctatttgcta aatattggaga accaggagaa gtttttatca
1081 acaaaggcaa aggattcgga tttattaagc ttgaattctag agctttgggt gaaattgcca
1141 aagccgaact ggatgatata cccatgagag gttagacagc tcgagttcgc tttgccacac
1201 atgctgctgc cctttctgtt cgtaattctt caccttatgt tccaatgaa ctgttggaag
1261 aagccttttag ccaatttggg cctattgaaa gggctgttgt aatagtggat gatcgtggaa
55 1321 gatctacagg gaaaggcatt gttgaatttg cttctaagcc agcagcaaga aaggcatttg

1381 aacgatgcag tgaaggtggt ttcttactga cgacaactcc tcgtccagtc attgtggaac
1441 cacttgaaca actagatgat gaagatggtc ttcctgaaaa acttgcccag aagaatccaa
1501 tgtatcaaaa ggagagagaa acccctactc gttttgccc gcatggcacg tttgagtacg
1561 aatattctca gcgatggaag tctttggatg aaatggaaaa acagcaaagg gaacaagttg
5 1621 aaaaaaacat gaaagatgca aaagacaaat tggaaagtga aatggaagat gcctatcatg
1681 aacatcaggc aaatcttttg cgccaagatc tgatgagacg acaggaagaa ttaagacgca
1741 tggaagaact tcacaatcaa gaaatgcaga aacgtaaaga aatgcaattg aggcaagagg
1801 aggaacgacg tagaagagag gaagagatga tgattcgtca acgtgagatg gaagaccaa
1861 tgaggcgcca aagagaggaa agttacagcc gaatgggcta catggatcca cgggaaagag
10 1921 acatgcgaat gggtagcgga ggagcaatga acatgggaga tccctatggg tcaggaggcc
1981 agaaatttcc acctctagga ggtggtggtg gcatagggtt tgaagctaat cctggcggtc
2041 caccagcaac catgagtggg tccatgatgg gaagtgcacat gcgtactgag cgctttgggc
2101 agggaggtgc ggggcctgtg ggtggacagg gtcctagagg aatggggcct ggaactccag
2161 caggatatgg tagagggaga gaagagtacg aaggcccaaa caaaaaaccc cgattttaga
15 2221 tgtgatattt aggccttcat tccagtttgt tttgtttttt tgtttagata ccaatctttt
2281 aaattcttgc atttttagtaa gaaagctatc tttttatgga tgttagcagt ttattgacct
2341 aatatttgta aatggtctgt ttgggcagggt aaaattatgt aatgcagtgt ttggaacagg
2401 agaatttttt tttccttttt atttctttat ttttctttt ttactgtata atgtccctca
2461 agtttatggc agtgtagctt gtgcactga atttccaaag tgtaccaatt tttttttttt
20 2521 tactgtgctt caaataaata gaaaaatagt tataaaaaaa aaaaaaaaaa aaaaaaaaaa
2581 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa

SEQ ID NO. 9

25

X16850

2021 bp mRNA linear

Human mRNA for myoblast cell surface antigen 24.1D5.

30 1 gaattcaaaa gactatttgc taaatatgga gaaccaggag aagtttttat caacaaaggc
61 aaaggattcg gatttattaa gcttgaatct agagcttttg ctgaaattgc caaagccgaa
121 ctggatgata ccccatgag aggtagacag ctteagagtc gctttgccac acatgctgct
181 gccctttctg ttcgtaatct ttcaccttat gtttccaatg aactgttgga agaagccttt
241 agccaatttg gtcctattga aagggtggtt gtaatagtgg atgatcgtgg aagatctaca
35 301 gggaaaggca ttggtgaatt tgcttctaag ccagcagcaa gaaaggcatt tgaacgatgc
361 agtgaagggtg ttttcttact gacgacaact cctcgtccag tcattgtgga accacttgaa
421 caactagatg atgaagatgg tcttcctgaa aaacttgccc agaagaatcc aatgtatcaa
481 aaggagagag aaaccctccc tcgttttgcc cagcatggca cgtttgagta cgaatattct
541 cagcgatgga agtctttgga tgaaatggaa aaacagcaaa gggaacaagt tgaaaaaac
40 601 atgaaagatg caaaagacaa attggaaagt gaaatggaag atgcctatca tgaacatcag
661 gcaaatcttt tgccccaaga tctgatgaga cgacaggaag aattaagacg catggaagaa
721 cttcacaatc aagaaatgca gaaacgtaa gaaatgcaat tgaggcaaga ggaggaacga
781 cgtagaagag aggaagagat gatgattcgt caacgtgaga tggaagaaca aatgaggcgc
841 caaagagagg aaagttacag ccgaatgggc tacatggatc cacgggaaag agacatgca
45 901 atgggtggcg gaggagcaat gaacatggga gatccctatg gttcaggagg ccagaaattt
961 ccacctctag gaggtggtgg tggcataggt tatgaagcta atcctggcgt tccaccagca
1021 accatgagtg gttccatgat gggaaagtga atgcgtactg agcgctttgg gcaggagggt
1081 gcggggcctg tgggtggaca gggtcctaga ggaatggggc ctggaactcc agcaggatat
1141 ggtagaggga gagaagagta cgaaggccca acaaaaaaac cccgatttta gatgtgatat
50 1201 ttaggctttc attccagttt gttttgtttt tttgtttaga taccaatctt ttaaattctt
1261 gcatttttagt aagaaagcta tctttttatg gatgttagca gtttattgac ctaatatttg
1321 taaatggtct gtttgggcag gtaaaattat gtaatgcagt gtttggaaca ggagaatttt
1381 ttttctttt tatttcttta tttttcttt tttactgtat aatgtccctc aagtttatgg
1441 cagtgtacct tgtgccactg aatttccaaa gtgtaccaat tttttttttt ttactgtgct
55 1501 tcaaataaat agaaaaatag ttataatatt gatcttcaac tttgccatc atgcttctat

1561 gcatattagg ctacgtattc cacattgaaa gcatgagagt gtctaggcct ttgaatggca
1621 tatgccattt ctgggaaatg catctggagg ctaagtattg ctttctacaa ataattgccc
1681 cctttgtttt aaaaagaaga aatgcatatt gaagtagttt gatgatttgt ttggcatata
1741 ggaagcacgc tgggtgctaag tatttttttaa atgggttatgt aagcaaagct gaactgtaaa
5 1801 tcttcaggaa tatgtattaa gattgtggaa tgggtgtaag acaattggta gggggtgaaa
1861 gtgggtttga ttaaattggat cttttatggc cctatgatct atcctttact tgaaagcttt
1921 tgaaaagtgg aaaggtcatt ttgttgcatt tccccatttc ttgttttttaa aagaccaaca
1981 aatctcaagc cctataaatg gcttgtattg aacccegaatt c

10

SEQ ID NO. 10

NP_000917

933 aa linear

15

progesterone receptor [Homo sapiens]

AAS00096

933 aa linear

progesterone receptor [Homo sapiens]

20

AAD01587

933 aa linear

progesterone receptor [Homo sapiens]

25

AAA60081

933 aa linear

progesterone receptor Homo sapiens

P06401

30

933 aa linear

Progesterone receptor (PR).

1 mtelkakgpr aphvaggpps pevgspllcr paagpfpgsq tsdtlpevsa ipisldgllf
61 prpcqgqdps dektqdqgs1 sdvegaysra eatrgaggss ssppekds gl lds vldtlla
35 121 psgpgqsqps ppacevtssw clfgpelped ppaapatqrv lspm srsgc vgdssgtaa
181 ahkvlprgls parqlllpas esphwsgapv kpspqaaave veeedssese esagp1lkkgk
241 pralggaaag ggaaacppga aaggvalvpk edsrfisaprv alveqdapma pgrsplattv
301 mdfihvpilp lnhallaart rqlledesy d ggagaasafa pprtspcass tpvavgd fdp
361 cayppdaepk ddayplysdf qppalkikee eegaeasars prsylvagan paafpdfplg
40 421 pppplpprat psrpgeaavt aapasasvss asssgstlec ilykaegapp qggpfapppc
481 kapgasgcll prdglpetsa saaaagaapa lypalglngl pqlgyqaavl keglpqvypp
541 ylanylrdse asqspqysfe slpqkiclic gdeasgchyg vltcgsckvf fkramegqhn
601 ylcagrndci vdkirrknop acrlrkccqa gmvlggrkfk kfnkvrvvra ldavalpqp1
661 gvpnesqals qrftfsggqd iqlippllnl lmsiepdviy aghdntkpd t sssl1tslnq
45 721 lgerqlslsvv kwskslpgr nlhiddqitl iqyswmslmv fglgwrsykh vsgqmlyfap
781 dlilneqrmk essfyslclt mwqipqefvk lqvsqeeflc mkvlll1nti pleglrsqtq
841 feemrssyir elikaiglrq kgvvsssqrf yqltkl1dnl hdlvkqlhly clntfigsra
901 lsvefpemms eviaaqlpki lagmvkpllf hkk

50

SEQ ID NO. 11

BAB91074

831 aa linear

55

delta 4 progesterone receptor [Homo sapiens]

```

1 mtelkakgpr aphvaggpps pevgspllcr paagpfpgsq tsdtlpevsa ipisldgllf
61 prpcqgqgps dektqdqqs1 sdvegaysra eatrgaggss ssppekds gl lds vldtlla
121 psgpggsgps ppacvtssw clfgpelped ppaapatqrv lsplmsrsgc kvgdssgtaa
5 181 ahkvlprgls parqlllpas esphwsgapv kpspqaaave veeedgsese esagpllkkgk
241 pralggaaag ggaaavppga aaggvalvpk edsrf saprv alveqdapma pgrsplattv
301 mdfi hvpilp lnhallaart rqlledesy d ggagaasafa pprsspcass t p vavgd f p d
361 cayppdaepk ddayplysdf qppalkikee eegaeasars prsylvagan paafp d f p l g
421 pppplpprat psrpgeaavt aapasasvss asssgstlec ilykaegapp qggpfapppc
10 481 kapgasgcll prdglpsta saaaagaapa lypalglngl pqlgyqaavl keglpqvypp
541 ylnylrpdse asqspqysfe slpqkiclic gdeasgchyg vltcgsckvf fkramegqhn
601 ylcagrndci vdkirrkncp acrlrkccqa gmvlggfrnl hiddqitliq yswmslmvfg
661 lgwrsykhvs ggmlyfapdl ilneqrmkes sfyslcltmw qipqefvklq vsqeeflcmk
721 vllllntipl eglrsqtqfe emrssyirel ikaiglrqkg vvsssqrifyq ltklldnlhd
15 781 lvkqlhlycl ntfigsrals vefpemmsev iaaglpkila gmvkpllfhk k

```

SEQ ID NO. 12

BAC06585

20 695 aa linear
Progesterone receptor [Homo sapiens]

```

1 mtelkakgpr aphvaggpps pevgspllcr paagpfpgsq tsdtlpevsa ipisldgllf
61 prpcqgqgps dektqdqqs1 sdvegaysra eatrgaggss ssppekds gl lds vldtlla
25 121 psgpggsgps ppacvtssw clfgpelped ppaapatqrv lsplmsrsgc kvgdssgtaa
181 ahkvlprgls parqlllpas esphwsgapv kpspqaaave veeedgsese esagpllkkgk
241 pralggaaag ggaaavppga aaggvalvpk edsrf saprv alveqdapma pgrsplattv
301 mdfi hvpilp lnhallaart rqlledesy d ggagaasafa pprsspcass t p vavgd f p d
361 cayppdaepk ddayplysdf qppalkikee eegaeasars prsylvagan paafp d f p l g
30 421 pppplpprat psrpgeaavt aapasasvss asssgstlec ilykaegapp qggpfapppc
481 kapgasgcll prdglpsta saaaagaapa lypalglngl pqlgyqaavl keglpqvypp
541 ylnylrpdse asqspqysfe slpqkiclic gdeasgchyg vltcgsckvf fkramegqhn
601 ylcagrndci vdkirrkncp acrlrkccqa gmvlggfrnl hiddqitliq yswmslmvfg
661 lgwrsykhvs ggmlyfapdl ilndsfgrat ksnpv
35

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SEQ ID NO. 13

BAC11011

40 764 aa linear
delta 3+6/2 progesterone receptor [Homo sapiens].

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1 mtelkakgpr aphvaggpps pevgspllcr paagpfpgsq tsdtlpevsa ipisldgllf
61 prpcqgqgps dektqdqqs1 sdvegaysra eatrgaggss ssppekds gl lds vldtlla
45 121 psgpggsgps ppacvtssw clfgpelped ppaapatqrv lsplmsrsgc kvgdssgtaa
181 ahkvlprgls parqlllpas esphwsgapv kpspqaaave veeedgsese esagpllkkgk
241 pralggaaag ggaaavppga aaggvalvpk edsrf saprv alveqdapma pgrsplattv
301 mdfi hvpilp lnhallaart rqlledesy d ggagaasafa pprsspcass t p vavgd f p d
361 cayppdaepk ddayplysdf qppalkikee eegaeasars prsylvagan paafp d f p l g
50 421 pppplpprat psrpgeaavt aapasasvss asssgstlec ilykaegapp qggpfapppc
481 kapgasgcll prdglpsta saaaagaapa lypalglngl pqlgyqaavl keglpqvypp
541 ylnylrpdse asqspqysfe slpqkiclic gdeasgchyg vltcgsckvf fkramegrkf
601 kkfknvrvvr aldavalpqp vgvpnescal sqrttfspgq diqlipplin llmsiepdvi
661 yaghdntkpd tsssltsln qlgerqlsv vkwskslpgf rnlhiddqit liqyswmslm
55 721 vfglgwrsyk hvsggmlyfa pdlilneshr slssfklakk sssv

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SEQ ID NO.14

5 BAC11012
690 aa linear
delta4+6/2 progesterone receptor [Homo sapiens]

1 mtelkakgpr aphvaggpps pevgspllcr paagpfpgsq tsdtlpevsa ipisldgllf
10 61 prpcqgqdps dektqdqql sdvegaysra eatrgaggss ssppekds gl lds vldtlla
121 psgpggsqps ppacevtssw clfgpelped ppaapatqrv lsplmsrsgc kvgdssgtaa
181 ahkvlprgls parqlllpas esphwsgapv kpspqaaave veeedgsese esagpllkkgk
241 pralggaaag ggaaavppga aaggvalvpk edsrf saprv alveqdapma pgrsplattv
301 mdfi hvpilp lnhallaart rqlledesy d ggagaasafa pprsspcass tpvavgd fdp
15 361 cayppdaepk ddayplysdf qppalkikee eegaeasars prsylvagan paafpdfplg
421 pppplpprat psrpgeaavt aapasasvss asssgstlec ilykaegapp qggpfapppc
481 kapgasgcll prdglpsta saaaagaapa lypalglngl pqlgyqaavl keglpqvypp
541 ylnylrpdse asqspqysfe slpqkiclic gdeasgchyg vltcgsckvf fkramegqhn
601 ylcagrndci vdkirrkncp acrlrkccqa gmvlggfrnl hiddqitliq yswmslmvfg
20 661 lgwrsykhvs gqmlyfapdl ilneqsivts

SEQ ID NO.15

25 BAC11013
803 aa linear
delta 6/2 progesterone receptor [Homo sapiens].

1 mtelkakgpr aphvaggpps pevgspllcr paagpfpgsq tsdtlpevsa ipisldgllf
30 61 prpcqgqdps dektqdqql sdvegaysra eatrgaggss ssppekds gl lds vldtlla
121 psgpggsqps ppacevtssw clfgpelped ppaapatqrv lsplmsrsgc kvgdssgtaa
181 ahkvlprgls parqlllpas esphwsgapv kpspqaaave veeedgsese esagpllkkgk
241 pralggaaag ggaaavppga aaggvalvpk edsrf saprv alveqdapma pgrsplattv
301 mdfi hvpilp lnhallaart rqlledesy d ggagaasafa pprsspcass tpvavgd fdp
35 361 cayppdaepk ddayplysdf qppalkikee eegaeasars prsylvagan paafpdfplg
421 pppplpprat psrpgeaavt aapasasvss asssgstlec ilykaegapp qggpfapppc
481 kapgasgcll prdglpsta saaaagaapa lypalglngl pqlgyqaavl keglpqvypp
541 ylnylrpdse asqspqysfe slpqkiclic gdeasgchyg vltcgsckvf fkramegqhn
601 ylcagrndci vdkirrkncp acrlrkccqa gmvlggrkfk kfnkvrvvra ldavalppqv
40 661 gvpnesqals qrftfsgqd iqlipplinl lmsiepdviy aghdntkpd t sssltslnq
721 lgerqlslsvv kwkslpgrf nhiddqitl iqyswmslmv fglgwrsykh vegqmlyfap
781 dlilneshrs lssfklakks ssv

45 SEQ ID NO. 16

FGQGGAGPVGGQGP

50 SEQ ID NO.17

CTGAGTC

55 SEQ ID NO. 18

YGEPEGEVFINKGK

5 SEQ ID NO. 19

GIVEFASKPAAR

10 SEQ ID NO. 20

FAQHGTEEYBYSQR

15 SEQ ID NO. 21

NP_076092 (Murine PSF)

1 msrdrfrsrg gggggfhrrg ggggrggldh frspppgmgf nqnrpgmpgs pggpkpplpp
20 61 ppphqqqqqp ppqppppqp pphqpppph pphqppppp qeskpvpqg pgsapgvssa
121 pppavsappa nppttgappg pgptptpppa vpstapggpp pstpsgsvst tppqtggppp
181 ppaggagpgp kpgpgpggpk ggkmpgggpk gggpgmgapg ghpkpphrpg geprggrqhh
241 apyhqqhhqg pppggpgprt eekisdsegf kanlsllrrp gektytqrer lfvgnlpadi
301 tedefkrlfa kygepgevfi nkgkgfgfik lesralaeia kaelddtpmr grqlrvrfat
25 361 haaalsvrnl epyvsnelle eafsqfgpie ravvivddrg rstgkgivef askpaarkaf
421 ercsegvfll tttprpvive pleqlddedg lpeklaqkn myqkeretpp rfaqhgtfey
481 eysqrwksld emekqqreqv eknmkdakdk lesemedayh ehqanllrqd lmrrqeelrr
541 meelhsqemq krkemqlrge eerrreeem mirqremeeq mrrqreesys rmgyndprer
601 dmrmggggtm nmgdpygsgg qkfpplgggg gigyeapgv ppatmegsamm gsdmrterfg
30 661 qggagpvvgg gprgmppgtp agygrgreey egpnkkprf

SEQ ID NO. 22

35 VRMIDVG